1646

RAW SEQUENCE LISTING   DATE: 04/08/2002
PATENT APPLICATION: US/09/714,792   TIME: 09:15:57

Input Set : N:\jumbos\09714792.raw.txt
Output Set: N:\CRF3\04082002\I714792.raw

**Does Not Comply
Corrected Diskette Needed**

do edit

```
        SEQUENCE LISTING
 4 (1) GENERAL INFORMATION:
 6        (i) APPLICANT: Collins, Mary
 7                       Donaldson, Debra
 8                       Fitz, Lori
 9                       Neben, Tamlyn
10                       Whitters, Matthew
11                       Wood, Clive
13       (ii) TITLE OF INVENTION: CYTOKINE RECEPTOR CHAIN
15      (iii) NUMBER OF SEQUENCES: 9
17       (iv) CORRESPONDENCE ADDRESS:
18            (A) ADDRESSEE: Genetics Institute, Inc.
19            (B) STREET: 87 CambridgePark Drive
20            (C) CITY: Cambridge
21            (D) STATE: MA
22            (E) COUNTRY: USA
23            (F) ZIP: 02140
25        (v) COMPUTER READABLE FORM:
26            (A) MEDIUM TYPE: Floppy disk
27            (B) COMPUTER: IBM PC compatible
28            (C) OPERATING SYSTEM: PC-DOS/MS-DOS
29            (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
31       (vi) CURRENT APPLICATION DATA:
C--> 32            (A) APPLICATION NUMBER: US/09/714,792
C--> 33            (B) FILING DATE: 16-Nov-2000
34            (C) CLASSIFICATION:
36     (viii) ATTORNEY/AGENT INFORMATION:
37            (A) NAME: Brown, Scott A.
38            (B) REGISTRATION NUMBER: 32,724
39            (C) REFERENCE/DOCKET NUMBER: GI5268
41       (ix) TELECOMMUNICATION INFORMATION:
42            (A) TELEPHONE: (617) 498-8224
43            (B) TELEFAX: (617) 876-5851
```

ERRORED SEQUENCES

```
46 (2) INFORMATION FOR SEQ ID NO: 1:
48        (i) SEQUENCE CHARACTERISTICS:
49            (A) LENGTH: 1525 base pairs
50            (B) TYPE: nucleic acid
51            (C) STRANDEDNESS: double
52            (D) TOPOLOGY: linear
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                   RAW SEQUENCE LISTING              DATE: 04/08/2002
                   PATENT APPLICATION:  US/09/714,792    TIME: 09:15:57

                   Input Set : N:\jumbos\09714792.raw.txt
                   Output Set: N:\CRF3\04082002\I714792.raw
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      54      (ii) MOLECULE TYPE: cDNA
      56     (iii) HYPOTHETICAL: NO
      59      (ix) FEATURE:
      60              (A) NAME/KEY: CDS
      61              (B) LOCATION: 256..1404
      64      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
E--> 66      GAATTCGGCA CGAGGGAGAG GAGGAGGGAA AGATAGAAAG AGAGAGAGAA          60
      67 AGATTGCTTG      60
E--> 69      CTACCCCTGA ACAGTGACCT CTCTCAAGAC AGTGCTTTGC TCTTCACGTA          120
      70 TAAGGAAGGA · 120
E--> 72      AAACAGTAGA GATTCAATTT AGTGTCTAAT GTGGAAAGGA GGACAAAGAG
      73 GTCTTGTGAT     180
E--> 75      AACTGCCTGT GATAATACAT TTCTTGAGAA ACCATATTAT TGAGTAGAGC
      76 TTTCAGCACA     240
E--> 78      CTAAATCCTG GAGAA ATG GCT TTT GTG CAT ATC AGA TGC TTG TGT TTC ATT
W--> 79 291
      80                   Met Ala Phe Val His Ile Arg Cys Leu Cys Phe Ile
      81                     1               5                  10
E--> 83      CTT CTT TGT ACA ATA ACT GGC TAT TCT TTG GAG ATA AAA GTT AAT CCT
W--> 84 339
      85      Leu Leu Cys Thr Ile Thr Gly Tyr Ser Leu Glu Ile Lys Val Asn Pro
W--> 86          15              20                  25
E--> 88      CCT CAG GAT TTT GAA ATA TTG GAT CCT GGA TTA CTT GGT TAT CTC TAT
W--> 89 387
      90      Pro Gln Asp Phe Glu Ile Leu Asp Pro Gly Leu Leu Gly Tyr Leu Tyr
W--> 91          30              35                  40
E--> 93      TTG CAA TGG AAA CCT CCT GTG GTT ATA GAA AAA TTT AAG GGC TGT ACA
W--> 94 435
      95      Leu Gln Trp Lys Pro Pro Val Val Ile Glu Lys Phe Lys Gly Cys Thr
W--> 96          45              50                  55              60
E--> 98      CTA GAA TAT GAG TTA AAA TAC CGA AAT GTT GAT AGC GAC AGC TGG AAG
W--> 99 483
      100     Leu Glu Tyr Glu Leu Lys Tyr Arg Asn Val Asp Ser Asp Ser Trp Lys
W--> 101                 65              70                  75
E--> 103     ACT ATA ATT ACT AGG AAT CTA ATT TAC AAG GAT GGG TTT GAT CTT AAT
W--> 104 531
      105     ·Thr Ile Ile Thr Arg Asn Leu Ile Tyr Lys Asp Gly Phe Asp Leu Asn
W--> 106                 80              85                  90
E--> 108     AAA GGC ATT GAA GGA AAG ATA CGT ACG CAT TTG TCA GAG CAT TGT ACA
W--> 109 579
      110     Lys Gly Ile Glu Gly Lys Ile Arg Thr His Leu Ser Glu His Cys Thr
W--> 111         95              100                 105
E--> 113     AAT GGA TCA GAA GTA CAA AGT CCA TGG ATA GAA GCT TCT TAT GGG ATA
W--> 114 627
      115     Asn Gly Ser Glu Val Gln Ser Pro Trp Ile Glu Ala Ser Tyr Gly Ile
W--> 116         110             115                 120
E--> 118     TCA GAT GAA GGA AGT TTG GAA ACT AAA ATT CAG GAC ATG AAG TGT ATA
W--> 119 675
      120     Ser Asp Glu Gly Ser Leu Glu Thr Lys Ile Gln Asp Met Lys Cys Ile
```

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              RAW SEQUENCE LISTING                    DATE: 04/08/2002
              PATENT APPLICATION:  US/09/714,792      TIME: 09:15:57

              Input Set : N:\jumbos\09714792.raw.txt
              Output Set: N:\CRF3\04082002\I714792.raw

W--> 121  125                      130                135                140
E--> 123   TAT TAT AAC TGG CAG TAT TTG GTC TGC TCT TGG AAA CCT GGC AAG ACA
W--> 124 723
     125   Tyr Tyr Asn Trp Gln Tyr Leu Val Cys Ser Trp Lys Pro Gly Lys Thr
W--> 126                      145                150                155
E--> 128   GTA TAT TCT GAT ACC AAC TAT ACC ATG TTT TTC TGG TAT GAG GGC TTG
W--> 129 771
     130   Val Tyr Ser Asp Thr Asn Tyr Thr Met Phe Phe Trp Tyr Glu Gly Leu
W--> 131                      160                165                170
E--> 133   GAT CAT GCC TTA CAG TGT GCT GAT TAC CTC CAG CAT GAT GAA AAA AAT
W--> 134 819
     135   Asp His Ala Leu Gln Cys Ala Asp Tyr Leu Gln His Asp Glu Lys Asn
W--> 136                      175                180                185
E--> 138   GTT GGA TGC AAA CTG TCC AAC TTG GAC TCA TCA GAC TAT AAA GAT TTT
W--> 139 867
     140   Val Gly Cys Lys Leu Ser Asn Leu Asp Ser Ser Asp Tyr Lys Asp Phe
W--> 141      190                195                200
E--> 143   TTT ATC TGT GTT AAT GGA TCT TCA AAG TTG GAA CCC ATC AGA TCC AGC
W--> 144 915
     145   Phe Ile Cys Val Asn Gly Ser Ser Lys Leu Glu Pro Ile Arg Ser Ser
W--> 146  205                      210                215                220
E--> 148   TAT ACA GTT TTT CAA CTT CAA AAT ATA GTT AAA CCA TTG CCA CCA GAA
W--> 149 963
     150   Tyr Thr Val Phe Gln Leu Gln Asn Ile Val Lys Pro Leu Pro Pro Glu
W--> 151                      225                230                235
E--> 153   TTC CTT CAT ATT AGT GTG GAG AAT TCC ATT GAT ATT AGA ATG AAA TGG
W--> 154 1011
     155   Phe Leu His Ile Ser Val Glu Asn Ser Ile Asp Ile Arg Met Lys Trp
W--> 156                      240                245                250
E--> 158   AGC ACA CCT GGA GGA CCC ATT CCA CCA AGG TGT TAC ACT TAT GAA ATT
W--> 159 1059
     160   Ser Thr Pro Gly Gly Pro Ile Pro Pro Arg Cys Tyr Thr Tyr Glu Ile
W--> 161      255                      260                265
E--> 163   GTG ATC CGA GAA GAC GAT ATT TCC TGG GAG TCT GCC ACA GAC AAA AAC
W--> 164 1107
     165   Val Ile Arg Glu Asp Asp Ile Ser Trp Glu Ser Ala Thr Asp Lys Asn
W--> 166      270                275                280
E--> 168   GAT ATG AAG TTG AAG AGG AGA GCA AAT GAA AGT GAA GAC CTA TGC TTT
W--> 169 1155
     170   Asp Met Lys Leu Lys Arg Arg Ala Asn Glu Ser Glu Asp Leu Cys Phe
W--> 171  285                      290                295                300
E--> 173   TTT GTA AGA TGT AAG GTC AAT ATA TAT TGT GCA GAT GAT GGA ATT TGG
W--> 174 1203
     175   Phe Val Arg Cys Lys Val Asn Ile Tyr Cys Ala Asp Asp Gly Ile Trp
W--> 176                      305                310                315
E--> 178   AGC GAA TGG AGT GAA GAG GAA TGT TGG GAA GGT TAC ACA GGG CCA GAC
W--> 179 1251
     180   Ser Glu Trp Ser Glu Glu Glu Cys Trp Glu Gly Tyr Thr Gly Pro Asp
W--> 181                      320                325                330
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        183    TCA AAG ATT ATT TTC ATA GTA CCA GTT TGT CTT TTC TTT ATA TTC CTT        1299
        184    Ser Lys Ile Ile Phe Ile Val Pro Val Cys Leu Phe Phe Ile Phe Leu
W--> 185                335                 340                 345
E--> 187    TTG TTA CTT CTT TGC CTT ATT GTG GAG AAG GAA GAA CCT GAA CCC ACA
W--> 188 1347
        189    Leu Leu Leu Leu Cys Leu Ile Val Glu Lys Glu Glu Pro Glu Pro Thr
W--> 190          350                 355                 360
E--> 192    TTG AGC CTC CAT GTG GAT CTG AAC AAA GAA GTG TGT GCT TAT GAA GAT
W--> 193 1395
        194    Leu Ser Leu His Val Asp Leu Asn Lys Glu Val Cys Ala Tyr Glu Asp
W--> 195          365                 370                 375                 380
E--> 197    ACC CTC TGT TAAACCACCA ATTTCTTGAC ATAGAGCCAG CCAGCAGGAG
W--> 198 1444
        199    Thr Leu Cys
E--> 202    TCATATTAAA CTCAATTTCT CTTAAAATTT CGAATACATC TTCTTGAAAA
        203 TCCAAAAAAA    1504
        205    AAAAAAAAAA AAAAACTCGA G                                               1525
        291 (2) INFORMATION FOR SEQ ID NO: 3:
        293        (i) SEQUENCE CHARACTERISTICS:
        294            (A) LENGTH: 1369 base pairs
        295            (B) TYPE: nucleic acid
        296            (C) STRANDEDNESS: double
        297            (D) TOPOLOGY: linear
        299        (ii) MOLECULE TYPE: cDNA
        301       (iii) HYPOTHETICAL: NO
        304        (ix) FEATURE:
        305            (A) NAME/KEY: CDS
        306            (B) LOCATION: 103..1245
        309        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
E--> 311    GGATCCGCGC GGATGAAGGC TATTTGAAGT CGCCATAACC TGGTCAGAAG
        312 TGTGCCTGTC        60
E--> 314    GGCGGGGAGA GAGGCAATAT CAAGGTTTTA AATCTCGGAG AA ATG GCT TTC
        315 GTT        114
        316                                                Met Ala Phe Val
        317                                                 1
E--> 319    TGC TTG GCT ATC GGA TGC TTA TAT ACC TTT CTG ATA AGC ACA ACA TTT
W--> 320 162
        321    Cys Leu Ala Ile Gly Cys Leu Tyr Thr Phe Leu Ile Ser Thr Thr Phe
W--> 322      5                  10                  15                  20
E--> 324    GGC TGT ACT TCA TCT TCA GAC ACC GAG ATA AAA GTT AAC CCT CCT CAG
W--> 325 210
        326    Gly Cys Thr Ser Ser Ser Asp Thr Glu Ile Lys Val Asn Pro Pro Gln
W--> 327                25                  30                  35
E--> 329    GAT TTT GAG ATA GTG GAT CCC GGA TAC TTA GGT TAT CTC TAT TTG CAA
W--> 330 258
        331    Asp Phe Glu Ile Val Asp Pro Gly Tyr Leu Gly Tyr Leu Tyr Leu Gln
W--> 332                40                  45                  50
E--> 334    TGG CAA CCC CCA CTG TCT CTG GAT CAT TTT AAG GAA TGC ACA GTG GAA
W--> 335 306
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                    RAW SEQUENCE LISTING               DATE: 04/08/2002
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                    Input Set : N:\jumbos\09714792.raw.txt
                    Output Set: N:\CRF3\04082002\I714792.raw


        336     Trp Gln Pro Pro Leu Ser Leu Asp His Phe Lys Glu Cys Thr Val Glu
W--> 337             55                  60                  65
E--> 339     TAT GAA CTA AAA TAC CGA AAC ATT GGT AGT GAA ACA TGG AAG ACC ATC
W--> 340 354
        341     Tyr Glu Leu Lys Tyr Arg Asn Ile Gly Ser Glu Thr Trp Lys Thr Ile
W--> 342             70                  75                  80
E--> 344     ATT ACT AAG AAT CTA CAT TAC AAA GAT GGG TTT GAT CTT AAC AAG GGC
W--> 345 402
        346     Ile Thr Lys Asn Leu His Tyr Lys Asp Gly Phe Asp Leu Asn Lys Gly
W--> 347         85                  90                  95                  100
E--> 349     ATT GAA GCG AAG ATA CAC ACG CTT TTA CCA TGG CAA TGC ACA AAT GGA
W--> 350 450
        351     Ile Glu Ala Lys Ile His Thr Leu Leu Pro Trp Gln Cys Thr Asn Gly
W--> 352                 105                 110                 115
E--> 354     TCA GAA GTT CAA AGT TCC TGG GCA GAA ACT ACT TAT TGG ATA TCA CCA
W--> 355 498
        356     Ser Glu Val Gln Ser Ser Trp Ala Glu Thr Thr Tyr Trp Ile Ser Pro
W--> 357                 120                 125                 130
E--> 359     CAA GGA ATT CCA GAA ACT AAA GTT CAG GAT ATG GAT TGC GTA TAT TAC
W--> 360 546
        361     Gln Gly Ile Pro Glu Thr Lys Val Gln Asp Met Asp Cys Val Tyr Tyr
W--> 362             135                 140                 145
E--> 364     AAT TGG CAA TAT TTA CTC TGT TCT TGG AAA CCT GGC ATA GGT GTA CTT
W--> 365 594
        366     Asn Trp Gln Tyr Leu Leu Cys Ser Trp Lys Pro Gly Ile Gly Val Leu
W--> 367             150                 155                 160
E--> 369     CTT GAT ACC AAT TAC AAC TTG TTT TAC TGG TAT GAG GGC TTG GAT CAT
W--> 370 642
        371     Leu Asp Thr Asn Tyr Asn Leu Phe Tyr Trp Tyr Glu Gly Leu Asp His
W--> 372     165                 170                 175                 180
E--> 374     GCA TTA CAG TGT GTT GAT TAC ATC AAG GCT GAT GGA CAA AAT ATA GGA
W--> 375 690
        376     Ala Leu Gln Cys Val Asp Tyr Ile Lys Ala Asp Gly Gln Asn Ile Gly
W--> 377                 185                 190                 195
E--> 379     TGC AGA TTT CCC TAT TTG GAG GCA TCA GAC TAT AAA GAT TTC TAT ATT
W--> 380 738
        381     Cys Arg Phe Pro Tyr Leu Glu Ala Ser Asp Tyr Lys Asp Phe Tyr Ile
W--> 382             200                 205                 210
E--> 384     TGT GTT AAT GGA TCA TCA GAG AAC AAG CCT ATC AGA TCC AGT TAT TTC
W--> 385 786
        386     Cys Val Asn Gly Ser Ser Glu Asn Lys Pro Ile Arg Ser Ser Tyr Phe
W--> 387             215                 220                 225
E--> 389     ACT TTT CAG CTT CAA AAT ATA GTT AAA CCT TTG CCG CCA GTC TAT CTT
W--> 390 834
        391     Thr Phe Gln Leu Gln Asn Ile Val Lys Pro Leu Pro Pro Val Tyr Leu
W--> 392             230                 235                 240
E--> 394     ACT TTT ACT CGG GAG AGT TCA TGT GAA ATT AAG CTG AAA TGG AGC ATA
W--> 395 882
        396     Thr Phe Thr Arg Glu Ser Ser Cys Glu Ile Lys Leu Lys Trp Ser Ile
```

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                    RAW SEQUENCE LISTING              DATE: 04/08/2002
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                    Input Set : N:\jumbos\09714792.raw.txt
                    Output Set: N:\CRF3\04082002\I714792.raw

W--> 397     245                  250                 255                 260
E--> 399     CCT TTG GGA CCT ATT CCA GCA AGG TGT TTT GAT TAT GAA ATT GAG ATC
W--> 400 930
     401     Pro Leu Gly Pro Ile Pro Ala Arg Cys Phe Asp Tyr Glu Ile Glu Ile
W--> 402                          265                 270                 275
E--> 404     AGA GAA GAT GAT ACT ACC TTG GTG ACT GCT ACA GTT GAA AAT GAA ACA
W--> 405 978
     406     Arg Glu Asp Asp Thr Thr Leu Val Thr Ala Thr Val Glu Asn Glu Thr
W--> 407                          280                 285                 290
E--> 409     TAC ACC TTG AAA ACA ACA AAT GAA ACC CGA CAA TTA TGC TTT GTA GTA
W--> 410 1026
     411     Tyr Thr Leu Lys Thr Thr Asn Glu Thr Arg Gln Leu Cys Phe Val Val
W--> 412                  295                 300                 305
E--> 414     AGA AGC AAA GTG AAT ATT TAT TGC TCA GAT GAC GGA ATT TGG AGT GAG
W--> 415 1074
     416     Arg Ser Lys Val Asn Ile Tyr Cys Ser Asp Asp Gly Ile Trp Ser Glu
W--> 417          310                 315                 320
E--> 419     TGG AGT GAT AAA CAA TGC TGG GAA GGT GAA GAC CTA TCG AAG AAA ACT
W--> 420 1122
     421     Trp Ser Asp Lys Gln Cys Trp Glu Gly Glu Asp Leu Ser Lys Lys Thr
W--> 422     325                 330                 335                 340
E--> 424     TTG CTA CGT TTC TGG CTA CCA TTT GGT TTC ATC TTA ATA TTA GTT ATA
W--> 425 1170
     426     Leu Leu Arg Phe Trp Leu Pro Phe Gly Phe Ile Leu Ile Leu Val Ile
W--> 427                  345                 350                 355
E--> 429     TTT GTA ACC GGT CTG CTT TTG CGT AAG CCA AAC ACC TAC CCA AAA ATG
W--> 430 1218
     431     Phe Val Thr Gly Leu Leu Leu Arg Lys Pro Asn Thr Tyr Pro Lys Met
W--> 432                  360                 365                 370
E--> 434     ATT CCA GAA TTT TTC TGT GAT ACA TGA AGACTTTCCA TATCAAGAGA
W--> 435 1265
     436     Ile Pro Glu Phe Phe Cys Asp Thr  *
W--> 437          375                 380
E--> 439     CATGGTATTG ACTCAACAGT TTCCAGTCAT GGCCAAATGT TCAATATGAG
     440     TCTCAATAAA    1325
     442     CTGAATTTTT CTTGCGAAAA AAAAAAAAAA AAATCCGCGG ATCC                    1369
     445  (2) INFORMATION FOR SEQ ID NO: 4:
     447       (i) SEQUENCE CHARACTERISTICS:
     448          (A) LENGTH: 380 amino acids
     449          (B) TYPE: amino acid
     450          (D) TOPOLOGY: linear
     452      (ii) MOLECULE TYPE: protein
     454      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
     456     Met Ala Phe Val Cys Leu Ala Ile Gly Cys Leu Tyr Thr Phe Leu Ile
     457     1                   5                   10                  15
     459     Ser Thr Thr Phe Gly Cys Thr Ser Ser Ser Asp Thr Glu Ile Lys Val
     460                  20                  25                  30
     462     Asn Pro Pro Gln Asp Phe Glu Ile Val Asp Pro Gly Tyr Leu Gly Tyr
     463                  35                  40                  45
```

```
465    Leu Tyr Leu Gln Trp Gln Pro Pro Leu Ser Leu Asp His Phe Lys Glu
466         50              55              60
468    Cys Thr Val Glu Tyr Glu Leu Lys Tyr Arg Asn Ile Gly Ser Glu Thr
469    65              70              75                  80
471    Trp Lys Thr Ile Ile Thr Lys Asn Leu His Tyr Lys Asp Gly Phe Asp
472             85              90                  95
474    Leu Asn Lys Gly Ile Glu Ala Lys Ile His Thr Leu Leu Pro Trp Gln
475         100             105                 110
477    Cys Thr Asn Gly Ser Glu Val Gln Ser Ser Trp Ala Glu Thr Thr Tyr
478         115             120                 125
480    Trp Ile Ser Pro Gln Gly Ile Pro Glu Thr Lys Val Gln Asp Met Asp
481         130             135                 140
483    Cys Val Tyr Tyr Asn Trp Gln Tyr Leu Leu Cys Ser Trp Lys Pro Gly
484    145             150             155                 160
486    Ile Gly Val Leu Leu Asp Thr Asn Tyr Asn Leu Phe Tyr Trp Tyr Glu
487             165             170                 175
489    Gly Leu Asp His Ala Leu Gln Cys Val Asp Tyr Ile Lys Ala Asp Gly
490         180             185                 190
492    Gln Asn Ile Gly Cys Arg Phe Pro Tyr Leu Glu Ala Ser Asp Tyr Lys
493         195             200                 205
495    Asp Phe Tyr Ile Cys Val Asn Gly Ser Ser Glu Asn Lys Pro Ile Arg
496         210             215                 220
498    Ser Ser Tyr Phe Thr Phe Gln Leu Gln Asn Ile Val Lys Pro Leu Pro
499    225             230             235                 240
501    Pro Val Tyr Leu Thr Phe Thr Arg Glu Ser Ser Cys Glu Ile Lys Leu
502             245             250             255
504    Lys Trp Ser Ile Pro Leu Gly Pro Ile Pro Ala Arg Cys Phe Asp Tyr
505             260             265             270
507    Glu Ile Glu Ile Arg Glu Asp Asp Thr Thr Leu Val Thr Ala Thr Val
508         275             280             285
510    Glu Asn Glu Thr Tyr Thr Leu Lys Thr Thr Asn Glu Thr Arg Gln Leu
511         290             295             300
513    Cys Phe Val Val Arg Ser Lys Val Asn Ile Tyr Cys Ser Asp Asp Gly
514    305             310             315                 320
516    Ile Trp Ser Glu Trp Ser Asp Lys Gln Cys Trp Glu Gly Glu Asp Leu
517             325             330             335
519    Ser Lys Lys Thr Leu Leu Arg Phe Trp Leu Pro Phe Gly Phe Ile Leu
520         340             345             350
522    Ile Leu Val Ile Phe Val Thr Gly Leu Leu Leu Arg Lys Pro Asn Thr
523         355             360             365
```
E--> 525   **Tyr Pro Lys Met Ile Pro Glu Phe Phe Cys Asp Thr** (*)
E--> 526   370   375   380
```

VERIFICATION SUMMARY                    DATE: 04/08/2002
PATENT APPLICATION:  US/09/714,792      TIME: 09:15:58

Input Set : **N:\jumbos\09714792.raw.txt**
Output Set: **N:\CRF3\04082002\I714792.raw**

```
L:32 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:33 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:66 M:254 E: No. of Bases conflict, Input:0 Counted:50 SEQ:1
M:254 Repeated in SeqNo=1
L:79 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:84 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:86 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:89 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:91 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:94 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:96 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:99 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:101 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:104 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:106 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:109 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:111 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:114 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:116 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:119 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:121 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:124 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:126 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:129 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:131 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:134 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:136 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:139 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:141 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:144 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:146 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:149 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:151 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:154 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:156 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:159 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:161 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:164 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:166 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:169 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:171 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:174 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:176 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:179 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:181 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:185 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:188 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:190 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
```

VERIFICATION SUMMARY
PATENT APPLICATION: **US/09/714,792**

DATE: 04/08/2002
TIME: 09:15:58

Input Set : **N:\jumbos\09714792.raw.txt**
Output Set: **N:\CRF3\04082002\I714792.raw**

```
L:193 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:195 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:198 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:311 M:254 E: No. of Bases conflict, Input:0 Counted:50 SEQ:3
M:254 Repeated in SeqNo=3
L:320 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:322 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:325 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:525 M:342 E: Invalid Stop Code On Error, STOP CODON:*
L:526 M:203 E: No. of Seq. differs, LENGTH:Input:380 Found:381 SEQ:4
L:536 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=5
L:551 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=6
L:566 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=7
L:581 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=8
L:596 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=9
```

STATISTICS SUMMARY   DATE: 04/08/2002
PATENT APPLICATION: US/09/714,792   TIME: 09:15:58

Input Set : **N:\jumbos\09714792.raw.txt**
Output Set: **N:\CRF3\04082002\I714792.raw**

Application Serial Number: US/09/714,792
Alpha or Numeric: Alpha
Application Class:
Application File Date: 11-16-2000
Art Unit: 1646
Software Application: PatentIN1.0
Total Number of Sequences: 9
Total Nucleotides: 2994
Total Amino Acids: 764
Number of Errors: 58
Number of Warnings: 100
Number of Corrections: 0

MESSAGE SUMMARY

203 **E:** 1 (No. of Seq. differs)
246 **W:** 5 (Invalid value of Alpha Sequence Header Field)
254 **E:** 56 (No. of Bases conflict)
342 **E:** 1 (Invalid Stop Code On Error)
336 **W:** 95 (Invalid Amino Acid Number in Coding Region)